

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: _____

Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/671,773A

DATE: 11/27/2002

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#11

Input Set : A:\EP.txt

Output Set: N:\CRF4\11272002\I671773A.raw

3 <110> APPLICANT: BAYER CORPORATION
 5 <120> TITLE OF INVENTION: Pituitary Adenylate Cyclase Activating Peptide (PACAP)
 Receptor 3 (R3)
 6 Agonists and Their Pharmacological Methods of Use
 8 <130> FILE REFERENCE: Bayer
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/671,773A
 C--> 10 <141> CURRENT FILING DATE: 2001-05-31
 10 <150> PRIOR APPLICATION NUMBER: 09/407,832
 11 <151> PRIOR FILING DATE: 1999-09-28
 13 <150> PRIOR APPLICATION NUMBER: 09/595,280
 14 <151> PRIOR FILING DATE: 2000-06-15
 16 <160> NUMBER OF SEQ ID NOS: 341
 18 <170> SOFTWARE: PatentIn version 3.1
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 21 <211> LENGTH: 28
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Artificial Sequence
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 28 <220> FEATURE:
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 30 <222> LOCATION: (28)..(28)
 31 <223> OTHER INFORMATION: AMIDATION
 34 <400> SEQUENCE: 1
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 37 1 5 10 15
 40 Met Ala Val Lys Lys Tyr Leu Asn Ser Ile Leu Asn
 41 20 25
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 38
 46 <212> TYPE: PRT
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 52 <220> FEATURE:
 53 <221> NAME/KEY: MOD_RES
 54 <222> LOCATION: (38)..(38)
 55 <223> OTHER INFORMATION: AMIDATION
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 61 1 5 10 15
 64 Met Ala Val Lys Lys Tyr Leu Ala Ala Val Leu Gly Lys Arg Tyr Lys
 65 20 25 30
 68 Gln Arg Val Lys Asn Lys

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74 <212> TYPE: PRT
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82 <222> LOCATION: (30)..(30)
83 <223> OTHER INFORMATION: AMIDATION
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88 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
89 1 5 10 15
92 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg
93 20 25 30
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98 <212> TYPE: PRT
99 <213> ORGANISM: Artificial Sequence
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105 <221> NAME/KEY: MOD_RES
106 <222> LOCATION: (39)..(39)
107 <223> OTHER INFORMATION: AMIDATION
110 <400> SEQUENCE: 4
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113 1 5 10 15
116 Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser
117 20 25 30
120 Ser Gly Ala Pro Pro Pro Ser
121 35
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134 <222> LOCATION: (1)..(1)
135 <223> OTHER INFORMATION: ACETYLATION
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140 <222> LOCATION: (31)..(31)
141 <223> OTHER INFORMATION: AMIDATION
144 <220> FEATURE:
145 <221> NAME/KEY: MISC_FEATURE

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146 <222> LOCATION: (17)..(17)
147 <223> OTHER INFORMATION: Nle
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152 His Ser Asp Ala Val Phe Thr Glu Asn Tyr Thr Lys Leu Arg Lys Gln
153 1 5 10 15
W--> 156 Xaa Ala Ala Lys Lys Tyr Leu Asn Asp Leu Lys Lys Gly Gly Thr
157 20 25 30
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162 <212> TYPE: PRT
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170 <222> LOCATION: (31)..(31)
171 <223> OTHER INFORMATION: AMIDATION
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177 <223> OTHER INFORMATION: ACETYLATION
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186 Leu Ala Ala Lys Lys Tyr Leu Asn Asp Leu Lys Lys Gly Gly Thr
187 20 25 30
190 <210> SEQ ID NO: 7
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200 <222> LOCATION: (1)..(1)
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210 Leu Ala Ala Lys Lys Tyr Leu Asn Asp Leu Lys Lys Gly Gly Thr
211 20 25 30
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216 <212> TYPE: PRT
217 <213> ORGANISM: Artificial Sequence
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222 <220> FEATURE:
223 <221> NAME/KEY: PEPTIDE

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224 <222> LOCATION: (1)..(31)
225 <223> OTHER INFORMATION:
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230 1 5 10 15
233 Leu Ala Ala Lys Lys Tyr Leu Asn Asp Leu Lys Lys Gly Gly Thr
234 20 25 30
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238 <211> LENGTH: 28
239 <212> TYPE: PRT
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248 <223> OTHER INFORMATION: Nle
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265 <222> LOCATION: (10)..(10)
266 <223> OTHER INFORMATION: CH3O-Y
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W--> 275 Xaa Ala Ala Lys Lys Tyr Leu Asn Asp Leu Lys Lys
276 20 25
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289 <222> LOCATION: (1)..(28)
290 <223> OTHER INFORMATION:
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294 His Ser Asp Ala Val Phe Thr Glu Asn Tyr Thr Lys Leu Arg Lys Gln
295 1 5 10 15
298 Leu Ala Ala Lys Lys Tyr Leu Asn Asp Leu Lys Lys
299 20 25

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Input Set : A:\EP.txt
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304 <212> TYPE: PRT
305 <213> ORGANISM: Artificial Sequence
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312 <222> LOCATION: (28)..(28)
313 <223> OTHER INFORMATION: AMIDATION
316 <400> SEQUENCE: 11
318 His Ser Asp Ala Val Phe Thr Asp Asn Tyr Thr Arg Leu Arg Lys Gln
319 1 5 10 15
322 Met Ala Val Lys Lys Tyr Leu Asn Ser Ile Lys Lys
323 20 25
326 <210> SEQ ID NO: 12
327 <211> LENGTH: 31
328 <212> TYPE: PRT
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
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335 <221> NAME/KEY: PEPTIDE
336 <222> LOCATION: (1)..(31)
337 <223> OTHER INFORMATION:
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341 His Ser Asp Ala Val Phe Thr Asp Asn Tyr Thr Arg Leu Arg Lys Gln
342 1 5 10 15
345 Met Ala Val Lys Lys Tyr Leu Asn Ser Ile Lys Lys Gly Gly Thr
346 20 25 30
349 <210> SEQ ID NO: 13
350 <211> LENGTH: 31
351 <212> TYPE: PRT
352 <213> ORGANISM: Artificial Sequence
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357 <220> FEATURE:
358 <221> NAME/KEY: PEPTIDE
359 <222> LOCATION: (1)..(31)
360 <223> OTHER INFORMATION:
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364 His Ser Asp Ala Val Phe Thr Glu Asn Tyr Thr Lys Leu Arg Lys Gln
365 1 5 10 15
368 Leu Ala Ala Lys Lys Tyr Leu Asn Asp Leu Leu Asn Gly Gly Thr
369 20 25 30
372 <210> SEQ ID NO: 14
373 <211> LENGTH: 31
374 <212> TYPE: PRT
375 <213> ORGANISM: Artificial Sequence

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 17
Seq#:9; Xaa Pos. 10, 17

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16
L:227 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8, Line#:225
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:16
L:292 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10, Line#:290
L:339 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12, Line#:337
L:362 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13, Line#:360
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L:408 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15, Line#:406
L:455 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17, Line#:453
L:478 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18, Line#:476
L:505 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19, Line#:503
L:528 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20, Line#:526
L:551 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21, Line#:549
L:574 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22, Line#:572
L:597 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23, Line#:595
L:620 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24, Line#:618
L:643 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25, Line#:641
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L:735 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29, Line#:733
L:758 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30, Line#:756
L:781 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31, Line#:779
L:804 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32, Line#:802
L:827 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33, Line#:825
L:850 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:34, Line#:848
L:873 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35, Line#:871
L:896 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:36, Line#:894
L:919 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:37, Line#:917
L:942 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:38, Line#:940
L:965 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:39, Line#:963
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L:1080 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:44, Line#:1078
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L:1306 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:54
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 L:4989 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:215
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L:5491 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:241
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L:5567 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:245
L:5586 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:246
L:5605 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:247
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